SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> ORTHOGONAL GENE SWITCHES

<130> ITR0041-PCT

<150> 60/514,362
<151> 2003-10-24

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 314
<212> PRT
<213> human

<400> 1

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Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Leu Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
```

```
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 2
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with a point mutation

<400> 2

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Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Met Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
```

Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
290 295 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305 310

<210> 3
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 3
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
1 5 10 15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
115 120 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225 230 235 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
245 250 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
260 265 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
275 280 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
290 295 300

Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305 310

<210> 4
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 4
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
1 5 10 15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
100 105 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
115 120 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
130 135 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225 230 235 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
245 250 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
260 265 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
275 280 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
290 295 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305 310

<210> 5
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 5

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 6
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 6

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190

His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 7
<211> 314

<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 7

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Met Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 8
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 8

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 9
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 9

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 10
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 10

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Ile Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 11
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 11

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 12
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 12

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp

            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val

305                 310
```

<210> 13
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 13

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 14
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 14

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 15
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 15

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 16
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 16

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 17
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 17

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 18
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 18

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 19
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 19

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 20
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 20

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Met Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 21
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 21

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 22
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 22

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 23
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 23

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Ile Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 24
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 24

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 25
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 25

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 26
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 26

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 27
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 27

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225                 230                 235                 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 28
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 28
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
1 5 10 15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
20 25 30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
35 40 45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
50 55 60
Leu Thr Asn Leu Ala Ala Arg Glu Leu Val His Met Ile Asn Trp Ala
65 70 75 80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
85 90 95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
100 105 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
115 120 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
130 135 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145 150 155 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
165 170 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
180 185 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
195 200 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
210 215 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Gly
225 230 235 240
Met Glu Val Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
245 250 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
260 265 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
275 280 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
290 295 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305 310

<210> 29
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 29

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 30
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 30

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Ile Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 31
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 31

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 32
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 32

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 33
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 33

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Met Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Met Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 34
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 34

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 35
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 35

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 36
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 36

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Ile Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Val Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 37
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 37

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285

Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 38
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 38

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 39
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 39

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Gly Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160

Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 40
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 40

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30
Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Leu Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 41
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> human sequence with point mutations

<400> 41

```
Ser Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met
 1               5                  10                  15
Ile Lys Arg Ser Lys Lys Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp
            20                  25                  30

Gln Met Val Ser Ala Leu Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser
        35                  40                  45
Glu Tyr Asp Pro Thr Arg Pro Phe Ser Glu Ala Ser Met Met Gly Leu
    50                  55                  60
Leu Thr Asn Leu Ala Asp Arg Glu Leu Val His Met Ile Asn Trp Ala
65                  70                  75                  80
Lys Arg Val Pro Gly Phe Val Asp Leu Thr Leu His Asp Gln Val His
                85                  90                  95
Leu Leu Glu Cys Ala Trp Met Glu Ile Leu Met Ile Gly Val Val Trp
            100                 105                 110
Arg Ser Met Glu His Pro Gly Lys Leu Leu Trp Ala Pro Asn Leu Leu
        115                 120                 125
Leu Asp Arg Asn Gln Gly Lys Cys Val Glu Gly Ala Val Glu Leu Phe
    130                 135                 140
Asp Met Leu Leu Ala Thr Ser Ser Arg Phe Arg Met Met Asn Leu Gln
145                 150                 155                 160
Gly Glu Glu Phe Val Cys Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly
                165                 170                 175
Val Tyr Thr Phe Leu Ser Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp
            180                 185                 190
His Ile His Arg Val Leu Asp Lys Ile Thr Asp Thr Leu Ile His Leu
        195                 200                 205
Met Ala Lys Ala Gly Leu Thr Leu Gln Gln Gln His Gln Arg Leu Ala
    210                 215                 220
Gln Leu Leu Leu Ile Leu Ser His Ile Arg His Met Ser Asn Lys Arg
225                 230                 235                 240
Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Val Val Pro Leu Tyr
                245                 250                 255
Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His Ala Pro Thr
            260                 265                 270
Ser Arg Gly Gly Ala Ser Val Glu Glu Thr Asp Gln Ser His Leu Ala
        275                 280                 285
Thr Ala Gly Ser Thr Ser Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr
    290                 295                 300
Gly Glu Ala Glu Gly Phe Pro Ala Thr Val
305                 310
```

<210> 42
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus human sequence

<400> 42
ggttaatatt aata 14

<210> 43
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> chimeric human sequence with point mutations

<400> 43

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Val | Ser | Lys | Leu | Ser | Gln | Leu | Gln | Thr | Glu | Leu | Leu | Ala | Ala | Leu |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Glu | Ser | Gly | Leu | Ser | Lys | Glu | Ala | Leu | Ile | Gln | Ala | Leu | Gly | Glu |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Pro | Gly | Pro | Tyr | Leu | Leu | Ala | Gly | Glu | Gly | Pro | Leu | Asp | Lys | Gly | Glu |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Ser | Cys | Gly | Gly | Gly | Arg | Gly | Glu | Leu | Ala | Glu | Leu | Pro | Asn | Gly | Leu |
| 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Glu | Thr | Arg | Gly | Ser | Glu | Asp | Glu | Thr | Asp | Asp | Asp | Gly | Glu | Asp |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Thr | Pro | Pro | Ile | Leu | Lys | Glu | Leu | Glu | Asn | Leu | Ser | Pro | Glu | Glu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ala | Ala | His | Gln | Lys | Ala | Val | Val | Glu | Thr | Leu | Leu | Gln | Glu | Asp | Pro |
| | | 100 | | | | | 105 | | | | | 110 | | | |
| Trp | Arg | Val | Ala | Lys | Met | Val | Lys | Ser | Tyr | Leu | Gln | Gln | His | Asn | Ile |
| | 115 | | | | | 120 | | | | | 125 | | | | |
| Pro | Gln | Arg | Glu | Val | Val | Asp | Thr | Thr | Gly | Leu | Asn | Gln | Ser | His | Leu |
| 130 | | | | | 135 | | | | | 140 | | | | | |
| Ser | Gln | His | Leu | Asn | Lys | Gly | Thr | Pro | Met | Lys | Thr | Gln | Lys | Arg | Ala |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Ala | Leu | Tyr | Thr | Trp | Tyr | Val | Arg | Lys | Gln | Arg | Glu | Val | Ala | Gln | Gln |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Phe | Thr | His | Ala | Gly | Gln | Gly | Gly | Leu | Ile | Glu | Glu | Pro | Thr | Gly | Asp |
| | | 180 | | | | | 185 | | | | | 190 | | | |
| Glu | Leu | Pro | Thr | Lys | Lys | Gly | Arg | Arg | Asn | Arg | Phe | Lys | Trp | Gly | Pro |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Ala | Ser | Gln | Gln | Ile | Leu | Phe | Gln | Ala | Tyr | Glu | Arg | Gln | Lys | Asn | Pro |
| 210 | | | | | 215 | | | | | 220 | | | | | |
| Ser | Lys | Glu | Glu | Arg | Glu | Thr | Leu | Val | Glu | Glu | Cys | Asn | Arg | Ala | Glu |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Cys | Ile | Gln | Arg | Gly | Val | Ser | Pro | Ser | Gln | Ala | Gln | Gly | Leu | Gly | Ser |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Asn | Leu | Val | Thr | Glu | Val | Arg | Val | Tyr | Asn | Trp | Phe | Ala | Asn | Arg | Arg |
| | | 260 | | | | | 265 | | | | | 270 | | | |

```
Lys Glu Glu Ala Phe Arg His Lys Leu Ala Asp Ile Lys Asn Ser Leu
        275                 280                 285
Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu Asp Ala
    290                 295                 300

Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro Phe Ser
305                 310                 315                 320
Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg Glu Leu
                325                 330                 335
Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val Asp Leu
            340                 345                 350
Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Met Glu Ile
        355                 360                 365
Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly Lys Leu
    370                 375                 380
Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys Cys Val
385                 390                 395                 400
Glu Gly Gly Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser Ser Arg
                405                 410                 415
Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu Lys Ser
            420                 425                 430
Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser Thr Leu
        435                 440                 445
Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp Lys Ile
    450                 455                 460
Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr Leu Gln
465                 470                 475                 480
Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser His Ile
                485                 490                 495
Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser Met Lys Cys
            500                 505                 510
Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp Ala
        515                 520                 525
His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val Glu Glu
    530                 535                 540
Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser His Ser
545                 550                 555                 560
Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro Ala Thr
                565                 570                 575
Val Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu
            580                 585                 590
Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys
        595                 600                 605
Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile
    610                 615                 620
Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln
625                 630                 635                 640
Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe

                645                 650                 655
Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu
            660                 665                 670
Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro
        675                 680                 685
```

```
Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro
    690                 695                 700
Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys
705                 710                 715                 720
Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu
                725                 730                 735
Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp
            740                 745                 750
Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln
        755                 760                 765
Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro
    770                 775                 780
Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala
785                 790                 795                 800
Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu
                805                 810                 815
Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp
            820                 825                 830
Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser
        835                 840
```

<210> 44
<211> 7
<212> PRT
<213> human

<400> 44
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Met Pro Lys Arg Pro Arg Pro
 1               5
```

<210> 45
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 45
ggaattcgtt gaccgggtct gctggagaca tg 32

<210> 46
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 46
ggaattcgag ctctgaacca gacccgactg tggcagggaa acc 43

<210> 47
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 47
gtccctgacg gccgaccaga tggtcagtgc cttgttggat gctgagccc 49

<210> 48
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 48
gtgctccatg gagcgccaga cgagaccaat catcaggatc tccatccagg c 51

<210> 49
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 49
caaggcaggc ctgaccctgc agcagcagca cc 32

<210> 50
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 50
gcatctccag cagcaggtca tagaggggca ccacgttctt gcacttcatg ctgtacagat 60
gctccatcac tttg 74

<210> 51
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 51
gcatctccag cagcaggtca tagaggggca ccacgttctt gcacttcatg ctgtacagca 60
cctccatgcc ttt 73

<210> 52
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 52
cttcagtgaa gcttcgatga tgggcttact gaccaacctg gcagccaggg 50

<210> 53
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 53
ctatgacctg ctgctggaga tgctggacg 29

<210> 54

<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 54
catatggtcg acgaattcgc ggccgcac 28

<210> 55
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 55
gcatctccag cagcaggtca tagaggggca ccacgttctt gcacttcatg ctgtacagat 60
gctccatgcg tttg 74

<210> 56
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 56
gtccaagatc tccacgatgc cctctacac 29

<210> 57
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 57
gatatccaag aacagcctgg ccttgtccct gacg 34

<210> 58
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 58
actagtgaat tcgactgtgg cagggaaacc ctctgcctcc c 41

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 59
ctgaccaacc tggcagacag 20

<210> 60
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 60
ggactcggtg gatatggtcc 20

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 61
gttcacatga tcaactgggc g 21

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> human sequence with added restriction site sequence

<400> 62
gagacttcag ggtgctggac 20